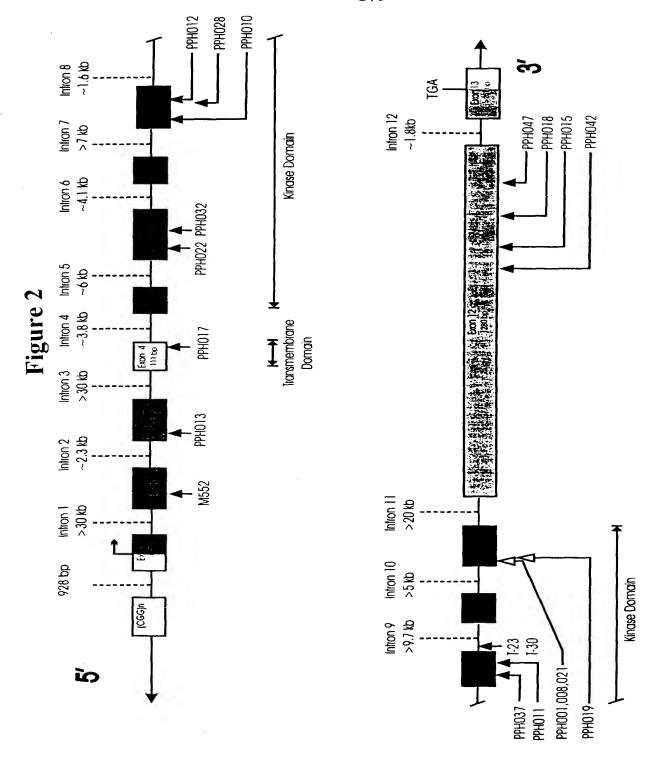


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CT TCG la Ser	GA TAT ly Cys	GT CCA er Pro	GA GAC ly Asp	CTG ATT	GGA TC1		GTT GG(GCA GTC	C MAC
ttcctttattttag	catattgatttatag	tttgttttcttttag	ttcctgttcttatag	ttaaaacacttgcag	ttttcctctatatag	aaattatccaaacag	actctaatttatcag	tctacaaatccacag	tactttgtcttacag	ctttctttctttaag
intron 1 (>30 kb)	intron 2 (~2.3 kb)	intron 3 (>30 kb)	intron 4 (~3.8 kb)	intron 5 (~6 kb)	intron 6 (~4.1 kb)	intron 7 (>7 kb)	intron 8 (~1.6 kb)	intron 9 (>9.7 kb)	intron 10 (>5 kb)	intron 11 (>20 kb)
gtgagtagctccggc	gcaagtgatactttc	gtaagtaaagtaacc	gtaaaaattaccatt	gtaagtttgccgtta	gtaagttcttcatag	gtaagatagtcaata	gtgagtgtatacaaa	gtaaaaactactgtc	gtaagaaaaactaa	gtaagaccctaaggg
GCT G Ala A	CAA G Gln G	CTC A Leu S	ACA G Thr G	TTG GAG Leu Glu	CCC AAT Pro Asn	GGA G Gly A	AGC GAG Ser Glu	CCA G Pro G	AGC CTG Ser Leu	GAA CG
EXON 1 (>460 bp)	EXON 2 (171 bp)	EXON 3 (171 bp)	EXON 4 (111 bp)	EXON 5 (92 bp)	EXON 6 (231 bp)	EXON 7 (115 bp)	EXON 8 (161 bp)	EXON 9 (148 bp)	EXON 10 (137 bp)	EXON 11 (173 bp)
	GCT G gtgagtagctccggc intron 1 (>30 kb)ttcctttattttag CT Ala A	GCT G gtgagtagctccggc intron 1 (>30 kb)ttcctttattttag Ala A CAA G gcaagtgatactttc intron 2 (~2.3 kb)catattgatttatag Gln G	GCT G gtgagtagctccggc intron 1 (>30 kb)tttcctttattttag CT last A la A last A last A last A last A gcaagtgatactttc intron 2 (~2.3 kb)catattgatttatag GA ly CTC A gtaagtaaagtaacc intron 3 (>30 kb)tttgttttcttttag GT leu S er	Ala A CAA G gcaagtgatacttc intron 2 (~2.3 kb)ttcctttattttag CIn G CIn G CTC A gtaagtaaagtaacc intron 3 (>30 kb)ttgttttcttttag Leu S ACA G gtaaaaattaccatt intron 4 (~3.8 kb)ttctgtttcttatag Thr G	Ala A CAA G gcaagtgatacttc intron 2 (~2.3 kb)ttcctttattttag Gln G CTC A gtaagtaaagtaacc intron 3 (>30 kb)ttgttttcttttag Leu S ACA G gtaagattgccatt intron 4 (~3.8 kb)ttctgttcttatag Thr G TTG GAG gtaagttgccgtta intron 5 (~6 kb)ttcaaaaacacttgcag	Ala A CAA G Gcaagtgatacttc intron 2 (~2.3 kb)catattgatttatag Gln G CTC A gtaagtaaagtaacc intron 3 (>30 kb)ttgttttcttttag Leu S ACA G gtaagaaattaccatt intron 4 (~3.8 kb)ttcctgttcttatag Thr G TTG GAG gtaagtttgccgtta intron 5 (~6 kb)ttaaaaacacttgcag Leu Glu CCC AAT gtaagttcttcatag intron 6 (~4.1 kb)tttcctctatatag	Ala A. CAA G gcaagtgatactttc intron 2 (~2.3 kb)catattgatttatag Gln G CTC A gtaagtaaagtaacc intron 3 (>30 kb)ttgtttcttttag Leu S ACA G gtaaaattaccatt intron 4 (~3.8 kb)ttctgttcttatag Thr G TTG GAG gtaagttgccgtta intron 5 (~6 kb)ttaaaaacacttgcag Leu Glu CCC AAT gtaagttctcatag intron 6 (~4.1 kb)tttcctctatatag Pro Asn GGA G gtaagatagtcaata intron 7 (>7 kb)aaattatccaaacag	Ala A CAA G gcaagtgatactttc intron 2 (-2.3 kb)catattgatttatag Gln G CTC A gtaagtaaagtaacc intron 3 (>30 kb)ttgttttcttttag Leu S ACA G gtaagattgccatt intron 4 (-3.8 kb)ttcctgttcttatag Thr G TTG GAG gtaagttgccgtta intron 5 (-6 kb)ttcctgttcttatag Leu Glu CCC AAT gtaagttcttcatag intron 6 (-4.1 kb)tttcctctatatag Pro Asn GGA G gtaagtgtatacaaa intron 7 (>7 kb)aaattatccaaacag G1y A AGC GAG gtgagtgtatacaaa intron 8 (-1.6 kb)actctaatttatcag ser Glu	Ala A CAA G gcaagtgatactttc intron 2 (-2.3 kb)catattgatttatag Gln G CTC A gtaagtaagtaacc intron 3 (>30 kb)ttgttttcttttag Leu S ACA G gtaagattgccatt intron 4 (-3.8 kb)ttctgttttctttag Thr G TTG GAG gtaagtttgccgtta intron 5 (-6 kb)ttcctgttcttatag Thr G CCC AAT gtaagttctcatag intron 6 (-4.1 kb)tttcctctatatag Pro Asn GGA G gtaagatagtcaata intron 7 (>7 kb)aaattatccaaacag Gly A AGC GAG gtaagatgtatacaaa intron 8 (-1.6 kb)actctaatttatcag Ser Glu CCA G Fro G Fro GA Fro G Fro G	Ala A. CAA G gcaagtgatacttc intron 2 (-2.3 kb)tttcctttattttag Gln G CTC A gtaagtaagtaacc intron 3 (>30 kb)tttgttttcttttag Leu S ACA G gtaaaaattaccatt intron 4 (-3.8 kb)ttcgttttcttttag TrG GAG gtaagttgccgtta intron 5 (-6 kb)ttcctgttcttatag Leu Glu CCC AAT gtaagttgccgtta intron 6 (-4.1 kb)tttcctctatatag Pro Asn GGA G gtaagttgtcaata intron 6 (-4.1 kb)tttcctctatatag GGA G gtaagttgtatacaaa intron 8 (-1.6 kb)aaattatccaaacag Gly A AGC GAG gtaagaaaactactgtc intron 8 (-1.6 kb)actctaatttatcag Ser Glu CCA G gtaagaaaactactgtc intron 9 (>9.7 kb)tctacaaatccacag Pro G

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igure 3

AMHR-II [Rattus norvegicus] TGFR-II (Rattus Norvegicus) BMPR-II (Xenopus lacvis) AMHR-II [Homo supiens] XSTK3 [Xenopus lacvis] BMPR-II [Mas musculus] TGFR-II [Mus musculus] TGFR-II [Homo sepiens] BMPR-II [Homo saplens] BMPR-II [Gallus gallus] ActR-II [Homo saplens] ActR-II [Oalhs gallus] DAF4 [C.elegans] ActR-II [sheep] Consensus R491W

LKETIEDCWD DAEA R LTAQCVEERMAEL LRELLEDCWDADPEA R LTAECWOORLAAL LKKVTEEMWDPEACA RITAGCAFARVWNH LCETIEECWDHDAEA R LSAGCVEERIIQM LRELLEDCWDADPEA R LTAECVQQRLAAL LCVTIEECWDHDAEA R LSAGCVEERISQI LKETIDDCWDQDAEA RILTAQCAEERMAEL VCETLTECWDHDPEA RILTAQCVAERFSEL VCETLTECWDHDPEA R LTAQCVAERFSEL VCETLTECWDHDPEA R LTAQCVAERFSEL LCETIEECWDHDAEA R LSAGCVGERITOM LKETIEDCWDQDAEA W LTAQCAEERMAEL LKETIEDCWDQDAEA RILTAQCAEERMAEL LKETIEDCWDQDAEA R LTAQCAEERMAEL LKETIEDCWDQDAEA RLTAQCAEERMAEL LCVTIEDCWDHDAEA R LSAGCVEERVSLI

Figure 4

Family #	#V#C/#N	Exon #	DNA Sequence Variation	Protein Sequence Variation
PPH001, 008 and 021	4/5/13	-	1471C>T	R491W
PPH010	2/0/1	8	1099-1103delGGGGA	E368fsX1
PPH015	8/1/9	12	2579delT	N861fsX10
PPH017	3/0/6	4	507-510delCTTTinsAAA	C169X
PPH018	3/2/4	13	2617C>T	R873X
PPH019	*5/0/1	=	1472G>A	R491Q
PPH022	2/0/0	9	690-691delAGinsT	K230fsX21
PPH011		6	1248-1251dclATTT	F417X
PPH012		∞	994C>T	R332X
PPH013		e	295T>C	C99R
PPH028		œ	1097delG	P366fsX8
PPH032		9	727G>T	E243X
PPH037		6	1214delA	D405fsX6
PPH042		12	2441-2442deIAC	H814fsX2
PPH047		12	2695C>T	R899X
M552		2	189-209del21	Del 64-70(STCYGLW)
PPH045		ĸ	296G>A	C99Y
PPH052		e	250T>C	C84R
PPH67-6701		∞	1040G>A	C347Y

1 ATGACTTCCT CSCTGCAGCG GCCCTGGCG GTGCCCTGGC TACCATGGAC TACTGAAGGA GCGACGTCGC CGGGACCGCC CACGGGACCG ATGGTACCTG TATTER LUL LU WS ST TIP AS AS AS ST GO AND GA GU AND LU CS 51 CATCCTGCTG GTCAGCACTG CGGCTGCTTC GCAGAATCAA GAACGGCTAT GTAGGACGAC CAGTCGTGAC GCGGCAGAAG CGTCTTAGTT CTTGCCGATA GTAGGACGAC CAGTCGTGAC GCGGACGAAG CGTCTTAGTT CTTGCCGATA TO QA BY THE WE AND PO TY GA GA AND GW NE GY GU ST AND 101 GTGCGTTTAA AGATCCGTAT CAGCAAGACC TTGGGATAGG TGAGAGTAGA CACGCAAATT TCTAGGCATA GTCGTTCTGG AACCCTATCC ACTCTCATCT THE ST HIS GW AND GY TI NE LU QS ST WE GY ST TIT QG TY TAGGAGGTAC TTTTACCCTG TTATAATACG AGCTTTCCAT CGTGGACGAT TAGGAGGTAC TTTTACCCTG TTATAATACG AGCTTTCCAT CGTGGACGAT TAGGAGGTAC TTTTACCCTG TTATAATACG AGCTTTCCAT CGTGGACGAT ACCGGAAACC CTCTTTAGTT TTCCCCTGTA TATAGAACAT TTTGTTCCTA TO QS TO ST HIS NE GY AND PO GA GU QS HIS TY GU GU QS WI 201 TGGCCTTTGG GAGAAATCAA AAGGGGACAT AAATCTTGTA AAACAAGGAT ACCGGAAACC CTCTTTAGTT TTCCCCTGTA TTTAGAACAT TTTGTTCCTA TO QS TO ST HIS NE GY AND PO GA GU QS HIS TY GU GU QS WI 202 TGGCTTAG CATTGGGAGT CCCCAAGAGT GTCACTATGA AGAATCGTTA CAACCAGAGT GTAACCTCTA GGGGTTCTCA CAGTGATACT TCTTACACAT THE THE THE POPO ST NE GH GW AND GY THE TY AND RE QS QS 301 GTAACTACCA CTCCTCCCTC AATTCAGAACT TGTATACC GTTTCTGCTG CATTGATGGT GAGGAGGGAG TTAAGTCTTA CACTTATGA AGAATCTGTTA THE THE POPO ST NE GW GW THE TY AND RE POPO POPO 303 GTAACTACCA CTCCTCCCTC CATTGAGAAT TGGAACATACC GTTTCTGCTG CATTGATGGT GAGGAGGGAG TTAAGTCTTA CCTTCTTATAGG CAAAGACCAC TCTTGATGGT GAGGAGGAG TTAAGTCTTA CCTTCTTATAGG CAAAGACCAC TCTTGATGGT GAGGAGGAG TTAAGTCTTA CCTTCTTATAGG CAAAGACCAC TCTTGATGGT GAGGAGGAG TTAAGTCTTA TATGAGAAT TTTCCACCTC AACCACCACA CACCACTCAGT CCCCTCCATT TATGATAGAT TTTCCACCTC AACCACCAC ACCACCACTCAGT CCCCTCCATT TATGAGAAT ACTATCAAGG TTAATTCATAC CTTTAGGATA ATGCAGAAA ACTATCAAGA TTTATTAGTACC TCTAAATACAT TACAGGTAAA ACTAATCAAGG TTAATTAGTAC GAAACACAT CACCCTCCATT TATGACTGAAAA ACTAATCAAGG TATATTAGCAA CCCATCAGT CACCTCCATT TATGACTGAAAA ACTAATCAAG TTATTAGCAAA CCTATGCTT CACCTCCATT GCCTTGCATT TATGATCTC TATATTATCTC GAAACACAT TACCTCTCTT AGACTGAAAA GAGACC		Met Thr Ser Ser Leu Gin Arg Pro Trp Arg Val Pro Trp Leu Pro Trp Thr
THE IDEA LOU NO SET THE ABO AND	1	ATGACTTCCT CGCTGCAGCG GCCCTGGCGG GTGCCCTGGC TACCATGGAC
CATCCTGCTG GTCAGCACTG CGGCTGCTTC GCAGAATCAA GAACGGCTAT GTAGGACGAC CAGTCGTGAC GCGACGAAG CGTCTTAGTT CTTGCCGATA OF MB PB US AND PPO TY ON GN AND LEU GY NE GY GU SS AG GTGGGTTTAA AGATCCCTAT CAGCAAGACC TTGGGATAGG TGAGAGTAGA CACGCAAATT TCTAGGCATA GTCGTTCTGG AACCCTATCC ACTCTACTCT		
GTAGGACGAC CAGTCGTGAC GCCGACGAAG CGTCTTAGTT CTTGCCGATA 10 Qs As Pre lis As Pro Ty Gn Gn As Liu Gy le Gy Gu Sa Ag 101 GTGCGTTTAA AGATCCGTAT CAGCAAGACC TTGGGATAGG TGAGAGTAGA CACGCAAATT TCTAGGCATA GTGGTTCTGG AACCCTATCC ACTCTCATCT 11 Ille Sa His Gu Asn Gy Tr le Lau Qs Sa Lis Gy Sa Tr Qs Ty 151 ATCTCTCATG AAAAATGGGAC AATATTATGC TCGAAAGAGTA GCACCTGCTA 17 Tr Qs Liu Tr Gu Lis Sa Lis Gy Asn Liu Va Lis Gn Gy Qs 201 TGGCCTTTGG GAGAAATCAA AAGGGGACAT AAATCTTGTA AAACAAGGAT ACCGGAAACC CTCTTTAGTT TTCCCCTGTA TTTTAGAACAT TTTGTTCCTA 11 Tr Gy Liu Tr Gu Lis Sa Lis Gy Asn Liu Va Lis Gn Gy Qs 201 TGGCCTTTGG GAGAAATCAA AAGGGGACAT AAATCTTGTA AAACAAGGAT ACCGGAAACC CTCTTTAGTT TTCCCCTGTA TTTTAGAACAT TTTGTTCCTA 11 Qs Tr Sa His Ne Gy Asn Pro Gn Gu Qs His Ty Gu Gu Qs Va 251 GTTGGTCTCA CATTGGAGAT CCCCAAGAGT GTCACTATGA AGAATGTGTA CAACCAGAGT GTAACCTCTA GGGGTTCTCA CAGTGATACT TCTTACACAT 11 Va Tr Tr Tr Tr Pro Pro Sa Lie Gn Asn Gy Tr Ty Ang Pro Qs Os 301 GTAACTACCA CTCCTCCCTC AATTCAGAAT GGAACATACC GTTTCTGCTG CATTGATGGT GAGGAGGGAG TTAAGTCTTA CCTTGTATAGG CAAAGACGAC 11 Qs Qs Sa Tr Asn Liu Qs Asn Va Asn Pro Tr Gu Asn Pro Pro Pro Pro Pro 251 TTGTAGCACA GATTTATGTA ATGTCAATCT TACGGAGAT TTTCCACCTC AACATCGTGT CTAAATACAT TACAGTTGAA ATGACTCTTA AAAGGTGGAG 11 Pro Asn Tr Tr Pro Liu Sa Pro Pro His Sa Pro Ang Asn Gu Tr 401 CTGACCACAC ACCACTCAGT CCACCTCATT CATTTAACCG AGATGAGACA 41 Pro Asn Tr Tr Pro Liu Sa Pro Pro His Sa Pro Ang Asn Gu Tr 401 CTGACCACAAC ACCACTCAGT CACCTCTGTT TATGTCTTTT TGATGAGACA ATTATTGTTTT TGGTGATCA GGTGGAGTAA GTAAATTGGC TCTATGTTTG TGTTGGCATT GTGTGGATCA GGTGGAGTAA GTAAATTGGC TCTATGTTTG 41 Pro Asn Tr Tr Pro Liu Sa Pro		
## OS AB PRO LIS ARD PRO TY ON GN ARD LEW GY NO GN ST AND GREATED STREAMS TRANSPORTED TO TOTAL CAGGACACT TTGGGATAGG TRAGGATAGA CACGCAAACT TCTAGGCATA GCGTTCTGG AACCCTATCC ACTCTCATCT NO ST HIS ST HIS GU AS GY NT NO NO NY	51	
GTGCCTTTAA AGATCCGTAT CAGCAAGACC TTGGGATAGG TGAGAGTAGA CACGCAAATT TCTAGGCATA GTCGTTCTGG AACCCTATCC ACTCTATCT	+1	
CACGCAAATT TCTAGGCATA GTCGTTCTGG AACCCTATCC ACTCTCATCT 1	101	
ATCTCTCATG AAAATGGGAC AATATTATGC TCGAAAGGTA GCACCTGCTA TAGAGAGTAC TTTTACCCTG TTATAATACG AGCTTTCCAT CGTGGACGAT 1 Ty Gy Lu Tp Gu Lys Ser Lys Gy Asp Ne Asp Lu Vs Lys Gn Gy Cys TGGCCTTTGG GAGAAATCAA AAGGGGACAT AAATCTTGTA AAACAAGGAT ACCGGAAACC CTCTTTAGTT TTCCCCTGTA TTTAGAACAT TTTGTTCCTA ACCGGAAACC CTCTTTAGTT TTCCCCTGTA TTTAGAACAT TTTGTTCCTA 1 O _S Tp Ser His Ne Gy Asp Po Gn Gu O _S His Ty Gu Gu O _S Vs 251 GTTGGTCTCA CATTGGAGAT CCCCAAGAGT GTCACTATGA AGAATGTGTA CAACCAGAGT GTAACCTCTA GGGGTTCTCA CAGTGATACT TCTTACACAT 1 Vs Tr Tr Tr Po Po Ser Ne Gn Su O _S Ni Ty Asp Pre O _S O _S 301 GTAACTACCA CTCCCCCCC AATTCAGAAT GGAACATACC GTTTCTGCTG CATTGATGGT GAGGAGGGAG TTAAGTCTTA CCTTGATAG CAAAGACCAC 1 O _S O _S Ser Tr Asp Lu O _S Asn Vs Asn Pre Tr Gu Asn Pre Pro Pro Pro 351 TTGTAGCACA GATTTATGTA ATGTCAACTT TACTGAGAAT TTTCCACCTC AACATCGGTG CTAAATACAT TACAGTTGAA ATGACTCTTA AAAGGTGGAG 1 Po Asp Tr Tr Pro Lu Ser Pro Pro His Ser Pre Asn Ag Asp Gu Tr 401 CTGACACAAC ACCACTCAGT CCACCTCATT CATTTAACCG AGATGACACA GACTGTGTTG TGGTGAGTCA GGTGGAGTAAA GTAAATTGGC TCTACTCTGT 1 Ne Ne Ne Asp Lu Ash Ser Vis Ser Vis Lu Ash Vis Lu Ne Vis Asp 451 ATAATCATTG CTTTGGCATC AGTCTCTGTA TTAGCTGTTT TGATGATGAC 1 Ne Lu O _S Pre Gy Ty Ang Mis Lu Tr Gly Asp Ang Lis Gn Gly Lu His 551 ATAATCATTG CTTTGGCATC AGTCTCTGTA TTAGCTGAAAA ACTATCAACG 1 Ash Lu O _S Pre Gy Ty Ang Mis Lu Tr Gly Asp Ang Lis Gn Gly Lu His 551 ACAGTATGAA CATTAGTGTA TACACTTCCC TCTGGCATTT GTTCCAGAGA 11 Ash Lu O _S Pre Gy Ty Ang Mis Lu Tr Gly Asp Ang Lis Gn Gly Lu His 551 ACAGTATGAA CATTAGTGCT CCGCCTCAGT CCGAACCCTC TCTTGATTTA 1 Asp Ash Lu Lis Lu Lu Gu Lu Ne Gy Ang Gy Ang Ty Gy Ash Vis 1 Asp Ash Lu Lis Lu Lu Gu Lu Ne Gy Ang Gy Ang Ty Gy Ash Vis 1 Asp Ash Lu Lis Gn Lu Ne Gu Ang Pre Ni Ash Vis Lis Vis Pre Ser Pre 651 ATATAAAGGC TCCTTGGATG GCGGACCCAT TCCTGGCATT ACCTCGTCA 1 Vis Ty Lis Gy Ser Lu Asp Gu Ang Pre Ni Ash Vis Lis Vis Pre Ser Pre 651 ATATAAAGGC TCCTTGGATG AGCGTCCAGT TCCTGTAAAA GTGTTTTCCT TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAAAAGGA 11 TTGCAAACCG TCAGAATTTT ATCAACGAAA		
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TY GY LEU TO GU LE SO LE GY ASD LE AND LEU VI LE GIN GY OS TGGCCTTTGG GAGAAATCAA AAGGGGACAT AAATCTTGTA AAACAAGGAT ACGGAAACC CTCTTTAGTT TTCCCCTGTA TTTAGAACAT TTTGTTCCTA 1 OS TO SO HIS LIE GY ASD PRO GIN GU OS HIS TY GU GU GU OS VI 251 GTTGGTCTCA CATTGGAGAT CCCCAAGAGT GTCACTATGA AGAATGTGTA CAACCAGAGT GTAACCTCTA GGGGTTCTCA CAGTGATACT TCTTACACAT 1 VI TIT TIT PRO PRO SO LIE GIN ASD GY TIT TY AND PRO OS OS 301 GTAACTACCA CTCCTCCCTC AATTCAGAAT GGAACATACC GTTTCTGCTG CATTGATGG GAAGAGGAGAC CATTGATGG GAAGAGGAGAC TAAGTTGATGG CAAAGAGGAC CATTGATGG GAGAGGAGGAG TTAAGTCTTA CCTTGTATGG CAAAGAGGAC CATTGATGGT GAGAGAGGAG TTAAGTCTTA CCTTGTATGG CAAAGAGGAC CATTGATGGT GAGAGAGGAGA TACGTGTTA ATGCACAT TACGAGAAT TTCCACCTC AACATCGTGT CTAAATACAT TACAGTTGAA ATGACTCTTA AAAGGTGGAG TAAACATCGTGT CTAAAATACAT TACAGTTGAA ATGACTCTTA AAAGGTGGAG GACATACC GACTGTGTT CTAAAATACAT TACAGTTGAA ATGACTCTTA AAAGGTGGAG GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TATAACTGGAGACA GACTGTGTT TOTTGAGACAA ACCACTCAGT CCACCTCATT CATTTAACCG AGATGGAGCA GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT LIE	151	ATCTCTCATG AAAATGGGAC AATATTATGC TCGAAAGGTA GCACCTGCTA
TGGCCTTTGG GAGAAATCAA AAGGGGACAT AAATCTTGTA AAACAAGGAT ACCGGAAACC CTCTTTAGTT TTCCCCTGTA TTTAGAACAT TTTGTTCCTA *1		
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+1 OS TIP SET HIS ILLE GIV ASP PRO GIN GLU OS HIS TY GLU OS VAI 251 GTTGGTCTCA CATTGGAGAT CCCCAAGAGT GTCACTATGA AGAATGTGTA CAACCAGAGT GTAACCTCTA GGGGTTCTCA CAGTGATACT TCTTACACAT +1 VAI TIV TIV PRO PRO SET ILLE GIN ASO GIV TIV TY AND PRE OS OS 301 GTAACCTACCA CTCCTCCCCTC AATTCAGAAT GGAACATACC GTTTCTGCTG CATTGATGGT GAGGAGGGAG TTAAGTCTTA CCTTGTATGG CAAAGACGAC +1 OS OS SET TIV ASP LAU OS ASO VAI ASO PRE TIV GLU ASO PRE PRO PRO PRO 251 TTGTAGCACA GATTTATGTA ATGTCAACTT TACTGAGAAT TTTCCACCTC AACATCGTGT CTAAATACAT TACAGTTGAA ATGACTCTTA AAAGGTGGAG +1 PRO ASP TIV TIV PRO LEU SE PRO PRO PRO PRO PRO PRO PRO ACCATCGTGT TGGTGAGTCA GTGGAGTAA GTAAATTGGC TCTACTCTGT GACTGTGTTT TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT 18 ILLE ILLE ILLE ALS ASS VAI SET VAI LEU ALS VAI LEU ILLE VAI AB 451 ATAATCATTG CTTTGGCATC AGTCTCTGTA TTAGCTGTTT TGATAGTTGC TATTAGTAAC GAAACCGTAG TCAGAGACAT AATTGACAAAA ACTATCAACG 41 AS LEU OS PRE GY TY AND MEL LEU TIV GY ASP AND US GIN GIV LEU HIS 501 CTTATGCTTT GGGTACCAGAA TGTTGACAGA AGACCGTAAA CAAGGTCTTC GAATACGAAA CCTATGTCTT ACAACTGTCC TCTGGCATTA GTTCCAGAAG 41 HIS SE ME ASO ME ME ME GU AS AND AS SE GU PRO SE LEU AND LEU 41 HIS SE ME ASO ME ME ME GU AS AND AND SE GU PRO SE LEU AND LEU 41 HIS SE ME ASO ME ME ME GU AS AND AND SE GU PRO SE LEU AND LEU 41 HIS SE ME ASO ME ME ME GU AS AND AND SE GU PRO SE LEU AND LEU 41 ASD AND LEU LIS LEU LEU GU LEU ILLE GY AND TY GY AND TY GY AND VEI 601 GATAATCTGA AACTGTTGGA GCAGCAGCAT CCGAACCCTC TCTTGGATCTA 41 VAI TY LIS GY SE LEU AND GU AND PRO VEI AND VEI AND VEI TGATAGTTCCT 651 ACAGTATGAA CTCTTGGAAG CTGACTAACCG GCTCCAGCTA ATGCAGAGAT 652 ATAATAAAGGC TCCTTGGAAG GCTGACTATGCC TGGGAGTAAA TACCTCGTCA 41 VAI TY LIS GY SE LEU AND GU AND PRO VEI AND VEI AND VEI PRO 651 ATATAAAAGGC TCCTTGGAAG GCAGCAGCAT TGCTGTAAAAA GTGTTTTCCT 653 ATATAAAAGGC TCCTTGGAAG AGCGTCAGAT TGCTGTAAAA GTGTTTTCCT 654 ATATAAAAGGC TCCTTGGAAG AGCGTCAGAT TGCTGTAAAAA GTGTTTTCCT 655 ATATAAAAGGC TCCTTGGAAG AGCGTCAGAT TGCTGTAAAAA GTGTTTTCCT 656 ATATAAAAGGC TCCTTGAATG AGCGTCAGATTTT ACAGCATTT CA	201	
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GAATACGAAA CCTATGTCTT ACAACTGTCC TCTGGCATTT GTTCCAGAAG +1 His Sør Met Asn Met Met Gu Ala Ala Sør Gu Pro Sør Lau Asp Lau 551 ACAGTATGAA CATGATGGAG GCAGCAGCAT CCGAACCCTC TCTTGATCTA TGTCATACTT GTACTACCTC CGTCGTCGTA GGCTTGGGAG AGAACTAGAT +1 Asp Asn Lau Lus Lau Lau Gu Lau Ille Gly Arg Gly Arg Tly Gly Ala Val 601 GATAATCTGA AACTGTTGGA GCTGATTGGC CGAGGTCGAT ATGGAGCAGT CTATTAGACT TTGACAACCT CGACTAACCG GCTCCAGCTA TACCTCGTCA +1 Va Ty Lus Gly Sør Lau Asp Gu Arg Pro Val Ala Val Lus Val Pre Sør Pre 651 ATATAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pre Ala Asn Arg Gin Asn Pre Ille Asn Gu Lus Asn Ille Ty Arg Val Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Lau Met Glu His Asp Asn Ille Ala Arg Pre Ille Val Gly Asp Glu Arg Val	+1 451	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT le le le le Ala Lau Ala Ser Val Ser Val Lau Ala Val Lau le Val Ala ATAATCATTG CTTTGGCATC AGTCTCTGTA TTAGCTGTTT TGATAGTTGC TATTAGTAAC GAAACCGTAG TCAGAGACAT AATCGACAAA ACTATCAACG
+1 His Ser Met Asn Met Met Gu Ala Ala Ser Gu Pro Ser Leu Asp Leu 551 ACAGTATGAA CATGATGAGG GCAGCAGCAT CCGAACCCTC TCTTGATCTA TGTCATACTT GTACTACCTC CGTCGTCGTA GGCTTGGGAG AGAACTAGAT +1 Asp Asn Leu Lijs Leu Leu Gu Leu IIe Gly Arg Gly Arg Ty Gly Ala Val 601 GATAATCTGA AACTGTTGGA GCTGATTGGC CGAGGTCGAT ATGGAGCAGT CTATTAGACT TTGACAACCT CGACTAACCG GCTCCAGCTA TACCTCGTCA +1 Va Ty Lijs Gly Ser Leu Asp Gu Arg Pro Val Ala Val Lijs Val Pre Ser Pre 651 ATATAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pre Ala Asn Arg Gin Asn Pre IIe Asn Gu Lijs Asn IIe Ty Arg Val Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Lau Met Gu His Asp Asn IIe Ala Arg Pre IIe Val Gly Asp Gu Arg Val	+1 451 +1	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT le le le le Als Leu Als Sør Val Sør Val Leu Als Val Leu le Val Als ATAATCATTG CTTTGGCATC AGTCTCTGTA TTAGCTGTTT TGATAGTTGC TATTAGTAAC GAAACCGTAG TCAGAGACAT AATCGACAAA ACTATCAACG Als Leu Os Pre Gly Ty Arg Ma Leu Tr Gly Asp Arg Lys Gin Gly Leu His
TGTCATACTT GTACTACCTC CGTCGTCGTA GGCTTGGGAG AGAACTAGAT ASD ASD LEU LIJS LEU LEU GU LEU IIIE GIJ AND GIJ AND TY GIJ ALD VAI GOTAATCTGA AACTGTTGGA GCTGATTGGC CGAGGTCGAT ATGGAGCAGT CTATTAGACT TTGACAACCT CGACTAACCG GCTCCAGCTA TACCTCGTCA 11 Va Ty Lijs Gij Ser Leu ASD GU AND PRO Val ALD VAI LIJS VAI PRO SER PRO 651 ATATAAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA 11 PRO ALD ASD AND GID ASD PRO IIIE ASD GU LIJS ASD IIIE TY AND VAI PRO 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA 11 LEU MAI GU HIS ASD ASD IIIE ALD AND PRO IIIE VAI GIJY ASD GU AND VAI	+1 451 +1	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
+1 ASD ASD LEU LIJE LEU LEU GU LEU IIIE GIY AND GIY AND TY GIY AND VAI 601 GATAATCTGA AACTGTTGGA GCTGATTGGC CGAGGTCGAT ATGGAGCAGT CTATTAGACT TTGACAACCT CGACTAACCG GCTCCAGCTA TACCTCGTCA +1 Val Ty Lije Giy Ser Leu ASD Gu Ang Pro Val Alb Val Lije Val Pro Ser Pro 651 ATATAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pro Alb Ash Ang Gin Ash Pro IIIe Ash Gu Lije Ash IIIe Ty Ang Val Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 LBU Mat Glu His Asp Ash IIIe Alb Ang Pro IIIe Val Giy Asp Giu Ang Val	+1 451 +1 501	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT le le le le Ala Lau Ala Ser Val Ser Val Lau Ala Val Lau le Val Ala
GATAATCTGA AACTGTTGGA GCTGATTGGC CGAGGTCGAT ATGGAGCAGT CTATTAGACT TTGACAACCT CGACTAACCG GCTCCAGCTA TACCTCGTCA +1 Va Ty Ls Gy Sa Lau Asp Gu Ang Pro Va Ab Va Ls Va Pre Sa Pre 651 ATATAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pre Ab Asn Ang Gin Asn Pre Ne Asn Gu Ls Asn Ne Ty Ang Va Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Lau Mat Gu His Asp Asn Ne Ab Ang Pre Ne Val Gly Asp Gu Ang Val	+1 451 +1 501	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT Ite Ite Ite Ala Lau Ala Ser Val Ser Val Lau Ala Val Lau Ite Val Ala ATAATCATTG CTTTGGCATC AGTCTCTGTA TTAGCTGTTT TGATAGTTGC TATTAGTAAC GAAACCGTAG TCAGAGACAT AATCGACAAA ACTATCAACG AB Lau Os Pre Gly Ty Arg Mar Lau Trr Gly Asp Arg Lys Gr Gly Lau Hs CTTATGCTTT GGATACAGAA TGTTGACAGG AGACCGTAAA CAAGGTCTTC GAATACGAAA CCTATGTCTT ACAACTGTCC TCTGGCATTT GTTCCAGAAG HIS Ser Mar Asr Mar Mar Glu Ala Ala Ser Glu Pro Ser Lau Asp Lau
CTATTAGACT TTGACAACCT CGACTAACCG GCTCCAGCTA TACCTCGTCA +1 Va Ty Ls Gy Sar Leu Asp Gu Ag Pro Va Ala Va Ls Va Pre Sar Pre 651 ATATAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pre Ala Asn Arg Gin Asn Pre Ne Asn Gu Ls Asn Ne Ty Arg Va Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Lau Mat Gu His Asp Asn Ne Ala Arg Pre Ne Va Gly Asp Gu Arg Val	+1 451 +1 501	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
+1 Va Ty Lys Gly Sar Leu Asp Gu Arg Pro Va Ala Val Lys Val Pre Sar Pre 651 ATATAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pre Ala Asn Arg Gin Asn Pre Ile Asn Gu Lys Asn IIe Ty Arg Val Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Leu Met Glu His Asp Asn IIe Ala Arg Pre IIe Val Gly Asp Glu Arg Val	+1 451 +1 501 +1 551	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
ATATAAAGGC TCCTTGGATG AGCGTCCAGT TGCTGTAAAA GTGTTTTCCT TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pre Ala Asn Arg Gin Asn Pre Ne Asn Gu Us Asn Ne Ne Ne Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 LEU MET Glu His Asp Asn Ne Ala Arg Pre Ne Val Gly Asp Glu Arg Val	+1 451 +1 501 +1 551	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
TATATTTCCG AGGAACCTAC TCGCAGGTCA ACGACATTTT CACAAAAGGA +1 Pre Ala Asn Arg Gin Asn Pre IIe Asn Giu Lis Asn IIe Ty Arg Val Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Lau Mat Glu His Asp Asn IIe Ala Arg Pre IIe Val Gly Asp Glu Arg Val-	+1 451 +1 501 +1 551 +1 601	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT e e e e e a a Lau Aa Ser Va Ser Va Lau Aa Va Lau Ile Va Aa ATAATCATTG CTTTGGCATC AGTCTCTGTA TTAGCTGTTT TGATAGTTGC
+1 Pre Ala Asn Arg Gln Asn Pre Ile Asn Gu Lus Asn Ile Ty Arg Val Pro 701 TTGCAAACCG TCAGAATTTT ATCAACGAAA AGAACATTTA CAGAGTGCCT AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Lau Mat Glu His Asp Asn Ile Ala Arg Pre Ile Val Gly Asp Glu Arg Val	+1 451 +1 501 +1 551 +1 601 +1	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
AACGTTTGGC AGTCTTAAAA TAGTTGCTTT TCTTGTAAAT GTCTCACGGA +1 Leu Met Glu His Asp Asn Ile Ala Arg Phe Ile Val Gly Asp Glu Arg Val	+1 451 +1 501 +1 551 +1 601 +1	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
+1 Leu Met Giu His Asp Asn lie Ala Arg Phe lie Val Gly Asp Giu Arg Val-	+1 451 +1 501 +1 551 +1 601 +1	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
	+1 451 +1 501 +1 551 +1 601 +1 651	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
751 TTCATCCAAC ATCACAACAT TCCCCCCTTT ATACTTCCAC ATCACACACT	+1 451 +1 501 +1 551 +1 601 +1 651	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT
AACTACCTTG TACTGTTGTA ACGGGCGAAA TATCAACCTC TACTCTCTCA	+1 451 +1 501 +1 551 +1 601 +1 651 +1 701	GACTGTGTTG TGGTGAGTCA GGTGGAGTAA GTAAATTGGC TCTACTCTGT

+1	-ValThr Aka Asp Gily Ang Met Gilu Tyr Leu Leu Val Met Gilu Tyr Tyr Pho Asm
801	CACTGCAGAT GGACGCATGG AATATTTGCT TGTGATGGAG TACTATCCCA
	GTGACGTCTA CCTGCGTACC TTATAAACGA ACACTACCTC ATGATAGGGT
+1	Asn Gily Ser Leu Cys Lys Tyr Leu Ser Leu His Thr Ser Asp Trip Val Ser
851	ATGGATCTTT ATGCAAGTAT TTAAGTCTCC ACACAAGTGA CTGGGTAAGC
	TACCTAGAAA TACGTTCATA AATTCAGAGG TGTGTTCACT GACCCATTCG
+1	Ser O _A s Arg Leu Ala His Ser Val Thr Arg Gly Leu Ala Ty Leu His Thr
901	TCTTGCCGTC TTGCTCATTC TGTTACTAGA GGACTGGCTT ATCTTCACAC
+1	AGAACGGCAG AACGAGTAAG ACAATGATCT CCTGACCGAA TAGAAGTGTG Thr Giu Leu Pro Aro Giv Aso His Tv Lus Pro Ala lie Ser His Aro Aso Leu
951	AGAATTACCA CGAGGAGATC ATTATAAACC TGCAATTTCC CATCGAGATT
+1	TCTTAATGGT GCTCCTCTAG TAATATTTGG ACGTTAAAGG GTAGCTCTAA Leu Asn Ser Arg Asn Val Leu Val Lys Asn Asp Gly Thr Oys Val Ike Ser
1001	TAAACAGCAG AAATGTCCTA GTGAAAAATG ATGGAACCTG TGTTATTAGT
1001	ATTTGTCGTC TTTACAGGAT CACTTTTTAC TACCTTGGAC ACAATAATCA
+1	Asp Pre Gly Leu Ser Met Arg Leu Thr Gly Ash Arg Leu Val Arg Pro Gly
1051	GACTTTGGAC TGTCCATGAG GCTGACTGGA AATAGACTGG TGCGCCCAGG
1031	CTGAAACCTG ACAGGTACTC CGACTGACCT TTATCTGACC ACGCGGGTCC
+1	-Gly Glu Glu Asp Asn Ala Ala Ile Ser Glu Val Gly Thr Ile Arg Tyr Met Ala
1101	GGAGGAAGAT AATGCAGCCA TAAGCGAGGT TGGCACTATC AGATATATGG
	CCTCCTTCTA TTACGTCGGT ATTCGCTCCA ACCGTGATAG TCTATATACC
+1	-Ala Pro Giu Val Leu Giu Giy Ala Val Asn Leu Arg Asp Cys Giu Ser Ala
1151	CACCAGAAGT GCTAGAAGGA GCTGTGAACT TGAGGGACTG TGAATCAGCT
	GTGGTCTTCA CGATCTTCCT CGACACTTGA ACTCCCTGAC ACTTAGTCGA
+1	Leu Lys Gin Val Asp Met Tyr Ala Leu Giy Leu lie Tyr Trop Giu lie Phe
1201	TTGAAACAAG TAGACATGTA TGCTCTTGGA CTAATCTATT GGGAGATATT
	AACTTTGTTC ATCTGTACAT ACGAGAACCT GATTAGATAA CCCTCTATAA
+1	Phe Met Arg Cys Thr Asp Leu Phe Pro Gly Glu Ser Val Pro Glu Tyr Gin Met
1251	TATGAGATGT ACAGACCTCT TCCCAGGGGA ATCCGTACCA GAGTACCAGA
	ATACTCTACA TGTCTGGAGA AGGGTCCCCT TAGGCATGGT CTCATGGTCT
+1	Met Ala Phe Gin Thr Gilu Val Gily Asn His Pro Thr Phe Gilu Asp Met Gin
1301	TGGCTTTTCA GACAGAGGTT GGAAACCATC CCACTTTTGA GGATATGCAG
+1	ACCGAAAAGT CTGTCTCCAA CCTTTGGTAG GGTGAAAACT CCTATACGTC
•	Val Leu Val Ser Ang Glu Lys Gh Ang Pro Lys Phe Pro Giu Ala Trp Lys
1351	GTTCTCGTGT CTAGGGAAAA ACAGAGACCC AAGTTCCCAG AAGCCTGGAA
+1	CAAGAGCACA GATCCCTTTT TGTCTCTGGG TTCAAGGGTC TTCGGACCTT Lys Glu Asn Sør Lau Ala Vai Arg Sør Lau Lys Glu Titr lie Glu Asp Oys Tip
1401	AGAAAATAGC CTGGCAGTGA GGTCACTCAA GGAGACAATC GAAGACTGTT
1401	TCTTTTATCG GACCGTCACT CCAGTGAGTT CCTCTGTTAG CTTCTGACAA
+1	-Trp Asp Gin Asp Ala Giu Ala Arg Leu Thr Ala Gin O ₁ 6 Ala Giu Giu Arg
1451	GGGACCAGGA TGCAGAGGCT CGGCTTACTG CACAGTGTGC TGAGGAAAGG
1431	CCCTGGTCCT ACGTCTCCGA GCCGAATGAC GTGTCACACG ACTCCTTTCC
+1	Met Ala Giu Leu Met Met lie Trp Giu Arg Asn Lys Ser Val Ser Pro Thr
1501	ATGGCTGAAC TTATGATGAT TTGGGAAAGA AACAAATCTG TGAGCCCAAC
	TACCGACTTG AATACTACTA AACCCTTTCT TTGTTTAGAC ACTCGGGTTG
+1	·Thr Val Asn Pro Met Ser Thr Ala Met Gln Asn Giu Arg Asn Leu Ser His Asn
1551	AGTCAATCCA ATGTCTACTG CTATGCAGAA TGAACGCAAC CTGTCACATA
	TCAGTTAGGT TACAGATGAC GATACGTCTT ACTTGCGTTG GACAGTGTAT

+1	i Asn Ang Ang Val Pro Lys. Ile Giy Pro Tyr Pro Asp Tyr Ser Ser Ser Ser
1601	ATAGGCGTGT GCCAAAAATT GGTCCTTATC CAGATTATTC TTCCTCCTCA
	TATCCGCACA CGGTTTTTAA CCAGGAATAG GTCTAATAAG AAGGAGGAGT
+1	
1651	TACATTGAAG ACTCTATCCA TCATACTGAC AGCATCGTGA AGAATATTTC
	ATGTAACTTC TGAGATAGGT AGTATGACTG TCGTAGCACT TCTTATAAAG
+1	Ser Ser Glu His Ser Met Ser Ser Thr Pro Leu Thr lie Gly Glu Lys Asn Arg
1701	CTCTGAGCAT TCTATGTCCA GCACACCTTT GACTATAGGG GAAAAAAACC
	GAGACTCGTA AGATACAGGT CGTGTGGAAA CTGATATCCC CTTTTTTTGG
+1	Ang Asn Ser lle Asn Tyr Giu Ang Gin Gin Ala Gin Ala Ang lle Pro Ser
1751	GAAATTCAAT TAACTATGAA CGACAGCAAG CACAAGCTCG AATCCCCAGC
	CTTTAAGTTA ATTGATACTT GCTGTCGTTC GTGTTCGAGC TTAGGGGTCG
+1	
1801	CCTGAAACAA GTGTCACCAG CCTCTCCACC AACACAACAA CCACAAACAC
	GGACTTTGTT CACAGTGGTC GGAGAGGTGG TTGTGTTGTT GGTGTTTGTG
+1	Thr Thr Gly Leu Thr Pro Ser Thr Gly Met Thr Thr Ile Ser Glu Met Pro Tyr
1851	CACAGGACTC ACGCCAAGTA CTGGCATGAC TACTATATCT GAGATGCCAT
	GTGTCCTGAG TGCGGTTCAT GACCGTACTG ATGATATAGA CTCTACGGTA
+1	Tyr Pro Asp Giu Thr Asn Leu His Thr Thr Asn Val Ata Gin Ser lie Giv
1901	ACCCAGATGA AACAAATCTG CATACCACAA ATGTTGCACA GTCAATTGGG
	TGGGTCTACT TTGTTTAGAC GTATGGTGTT TACAACGTGT CAGTTAACCC
+1	Pro Thr Pro Val Os Leu Gin Leu Thr Giu Gu Asp Leu Giu Thr Ash Lys
1951	CCAACCCCTG TCTGCTTACA GCTGACAGAA GAAGACTTGG AAACCAACAA
	GGTTGGGGAC AGACGAATGT CGACTGTCTT CTTCTGAACC TTTGGTTGTT
+1	The transfer of the contract o
	tys Leu Asp Pro Lys Giu Val Asp Lys Asn Leu Lys Giu Ser Ser Asp Giu Asn
+1 2001	Lys Lau Asp Pro Lys Glu Vai Asp Lys Asn Lau Lys Glu Sar Sar Asp Glu Asn GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA
	LIS LEU ASP PTO LIS GLU VII ASP LIS AST LEU LIS GLU SIT SIT ASP GLU AST GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT
2001	Lys Lau Asp Pro Lys Glu Vai Asp Lys Asn Lau Lys Glu Sar Sar Asp Glu Asn GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT Asn Lau Mat Glu His Sar Lau Lys Gin Pre Sar Gly Pro Asp Pro Lau Sar
2001	LIS LEU ASP PTO LIS GIU VAI ASP LIS ASP LEU LIS GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GIU HIS SET LEU LIS GIP PTO SET GIY PTO ASP PTO LEU SET ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC
2001	LIS LEU ASP PTO LIS GIU VAI ASP LIS ASP LEU LIS GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GIU HIS SET LEU LIS GIP PTO SET GLY PTO ASP PTO LEU SET ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG
2001 +1 2051 +1	LIS LEU ASP PTO LIS GIU VAI ASP LIS ASP LEU LIS GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GIU HIS SET LEU LIS GIP PTO SET GIV PTO ASP PTO LEU SET ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PTO LEU IIIO LIS LEU AIS VAI GIU ASP
2001 +1 2051	LIS LEU ASP PTO LIS GIU VAI ASP LIS AST LEU LIS GIU SET SET ASP GIU AST GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT AST LEU ME GIU HIS SET LEU LIS GIN FRE SET GIV PTO ASP PTO LEU SET ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PTO LEU IIIE LIS LEU AIS VAI GIU ASTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC
2001 +1 2051 +1 2101	LIS LEU ASP PTO LIS GIU VII ASP LIS AN LEU LIS GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GIU HIS SET LEU LIS GIN PRE SET GLY PRO ASP PRO LEU SET ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PRO LEU IIIE LIS LEU AIS VIS GIU AB AGTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG
2001 +1 2051 +1 2101 +1	LIS LEU ASP PTO LIS GIU VAI ASP LIS ASP LEU LIS GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GU HIS SET LEU LIS GN PRE SET GIV PRO ASP PRO LEU SET ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PRO LEU IIIE LIS LEU AIS VAI GIU ASP AGTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AAB TIT GIV GIV GIV ASP LEU IE
2001 +1 2051 +1 2101	LIS LEU ASP PTO LIS GIU VSI ASP LIS ASP LEU LIS GIU SST SST ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASPA LEU MSI GIU HIS SST LEU LIS GIP PTO SST GY PTO ASP PTO LEU SST ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SST TIT SST SST LEU LEU TY PTO LEU IIIO LIS LEU AIS VSI GIU ASP AGTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AIS TIT GIY GIP GIP ASP PTO TIT GIP TIT AS ASP GIY GIP AIS OS LEU LEU AACTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCCAA GCATGTTTGA
2001 +1 2051 +1 2101 +1	LIST LAU ASP PTO LIS GIU VAI ASP LIS AND LAU LIS GIU SAT SAT ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASPA LAU MAI GIU HIS SAT LAU LIS GIN PHE SAT GIV PHO ASP PHO LAU SAT ATCCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SAT TIT SAT SAT SAT LAU LAU TY PHO LAU IIIE LIS LAU AIS VAI GIU AB AGTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AB TIT GY GIN GIN ASP PHE TIT GIN TIT AIS ASP GIV GIN AIS OS LAU IE AACTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT
2001 +1 2051 +1 2101 +1 2151	LIS LEU ASP PTO LIS GIU VII ASP LIS AN LEU LIS GIU SE SE ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GU HIS SE LEU LIS GN PRE SE GIV PRO ASP PRO LEU SE ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SE TH SE SE SE LEU LEU TY PRO LEU IIIE LIS LEU AIS VIS GIU AIS AGTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AIS THY GIV GIN ASP PRE THY GIN THY AIS ASN GIV GIN AIS OS LEU IIE AACTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIE PRO ASP VIS LEU PRO THY GIN IIE TY PRO LEU PRO LIS GIN GIN ASN
2001 +1 2051 +1 2101 +1 2151	LIST LAU ASP PTO LIS GIU VII ASP LIS AND LIS LIS GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LIS ME GIU HIS SET LIS LIS GIN PRE SET GIV PTO ASP PTO LIS SET ASP LIS SET LIS LIS GIN PRE SET GIV PTO ASP PTO LIS SET ASP LIS LIS GIV PTO ASP PTO LIS SET ASP LIS
2001 +1 2051 +1 2101 +1 2151	LIST LAU ASP PTO LIS GIU VII ASP LIS AND LIS LIS GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASPA LIS ME GU HIS SET LIS LIS GIN PRE SET GIV PRO ASP PRO LIS SET ASPA LIS SET LIS LIS GIN PRE SET GIV PRO ASPA PRO LIS SET ASPA LIS ME GAGAGAGA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LIS LIS TY PRO LIS IIE LIS LIS AS VIS GIU ASPAGATACCT CTAGGCTTGATGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG ASA TIT GIV GIN ASPA PRE TIT GIN TIT AS ASPA GIV GIN ASPA CACTGGACAG CACGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIE PRO ASPA VIS LIS PRO TIT GIN IIE TY PRO LIS PRO LIS GIN GIN ASPA TTCCCTGATGT TCTGCCTTACT CAGATCTACT CTCTCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTTACCTGATGT TCTGCCTTACT CAGATCTATC CTCTCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTTAGCTATC CTCTCCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTTAGCTATC CTCTCCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTTAGATGA GGAGGAGGTT CGTCCTTTGGAGGATGA GCAGGAGTGA GCAGGAGAAC AAGGGACTACA AGACGGATGA GTCTTAGATAG GAGAGGGGGTT CGTCCTTTG
2001 +1 2051 +1 2101 +1 2151 +1 2201 +1	LIST LEU ASP PTO LIS GIU VI ASP LIS AN LEU LIS GIU SE SE ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GU HIS SE LEU LIS GN PRE SE GIV PRO ASP PRO LEU SE ATCTCATGGA GCACTCATGGA GCACTCATGGA GCACTCATGGA GCACTCATGGA GCACTCATGGA GCACTCATGGA GCACTCATGGA GCACTCATGGA GCACTCATGAGC CACGGGTCT GGGTGACTCG SE TH SE SE SE LEU LEU TY PRO LEU IIIE LIS LEU AIS VIS GIU ASP AGATCATAGAT CACGGGTCT GAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AS TH GIV GIN ASP PRE TH GIN TH AIS ASN GIV GIN AIS OS LEU IIIE AACTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT TILIE PRO ASP VIS LEU PRO TH GIN III TY PRO LEU PRO LIS GIN GIN ASN TTCCCTGATGT TCTGCCTACT CAGGATCTATC CTCTCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTAGATAG GAGAGGGGTT CGTCGTCTTG LEU PRO LIS AND FRO LIS ASN TH LIS ASN SE TH LIS
2001 +1 2051 +1 2101 +1 2151 +1 2201	LIST LEU ASP PTO LIS GIU VI ASP LIS AND LIS LIS GIU SE SE ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GU HIS SE LEU LIS GN PRE SE GIV PRO ASP PRO LEU SE ATCTCATGGA GCACTCATGGA GCACTCATGAGA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SE TH SE SE SE LEU LEU TY PRO LEU IIIE LIS LEU AIS VIS GIU ASP AGTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AAATTGGACAG GCATGTTTGA GATCGAACGA GAATGGGTGAG TATTTTGAAC GTCATCTTCG AAATTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIE PRO ASP VIS LEU PRO TH' GN IIE TY PRO LEU PRO LIS GN GIN ASN TTCCCTGATGT TCTGCCTACT CAGATCTATC CTCTCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTAGATAG GAGAGGGGTT CGTCGTCTTG LEU PRO LIS AND PRO TH' SE LEU PRO LEU ASN TH' LIS ASN SE TH' LIS CTTCCCCAAGA GACCTACAAAA ATTCAACAAA ATTCAACAAA
2001 +1 2051 +1 2101 +1 2151 +1 2201 +1 2251	LIST LAU ASP PTO LIS GIU VI ASP LIS AN LEU LIS GIU SE SE ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GU HIS SE LEU LIS GN PRE SE GY PTO ASP PTO LEU SE ATCTCCATGGA GCACTCCTCT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SE TH SE SE SE LEU LEU TY PTO LEU IIIE LIS LEU AIS VIS GU AIS AGATACTAGT CTAGGCTAGAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AGATCAAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AAATTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIE PTO ASP VIS LEU PTO TH' GN III AIS ASN GY GN AIS OS LEU III PTO ASP VIS LEU PTO TH' GN III TY PTO LEU PTO LIS GN GN ASN TTCCCTGAACC AAAGGGACTACA AGACGGATGA GTCTAGATAG GAGGGGGTT CGTCGTTTG LEU PTO LIS AG PTO TH' SE LEU PTO LEU ASN TH' LIS ASN SE TH' LIS CTTCCCCAAGA GACCTACTAGA GACGGATGAC TTTGCCCTAAAA ATTCAACAAA GAAGGGGTTC CTGGATGATCA TTTGCCCTAAGA GACCGAAAA ATTCAACAAA GAAGGGGTTC CTGGATGATCA AAACGGAAAC TTTGCCCTAAAA ATTCAACAAAA GAAGGGGTTC CTGGATGATCA AAACGGAAAC TTTGCCCAAAAA ATTCAACAAAA GAAGGGGTTC CTGGATGATCA AAACGGAAAC TTTGCCCTAAAA ATTCAACAAAA GAAGGGGTTC CTGGATGATCA TTTGCCTTTTG AACACCAAAAA ATTCAACAAAA GAAGGGGTTC CTGGATGATCA TTTGCCTTTTG AACACCAAAAA ATTCAACAAAA GAAGGGGTTC CTGGATGATCA CTGGGTTCTT TAAGTTGTTT
2001 +1 2051 +1 2101 +1 2151 +1 2201 +1 2251	LIVE LEU ASP PTO LIVE GIU VII ASP LIVE AND LIVE GIU SET SET ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GU HIS SET LEU LIVE GIN PRE SET GIV PTO ASP PTO LEU SET ATTCTCATGGA GCACTCCTCT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PTO LEU IIIE LIVE LEU AIS VIS GIU ARP AGTACTAGT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AAATTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIVE PTO ASP VIS LEU PTO TIT GIN III AS AST GIV GIN ASP GAGGACTACA AGACGGATGA GTCTTAGCTGT TCTCCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTAGATAG GAGGAGGGTT CGTCCTTGG AAAGGACTACA AGACGGATGA GTCTAGATAG GAGGAGGGTT CGTCGTTTG LEU PTO LIVE AND PTO TIT GIN III TY PTO LEU PTO LIVE GAGGAGAAC AAGGGACTACA AGACGGATGA GTCTAGATAG GAGAGGGGTT CGTCGTCTTG LEU PTO LIVE AND PTO TIT SET LEU PTO LEU AST TIT LIVE AST SET TIT LIVE GUI PTO AND LIVE PTO AND LIVE GIN VISIT CTTCCCCAAGA GACCTACAAAA CTTTCCCCAAAGA GAACGGATGAT CTTCCCCAAAAA ATTCAACAAA GAAGGGGTTCT CTGGATGATC AAACCGGAAAC TTTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE PTO AND LIVE PTO LIVE SET AST LIVE LIVE GIN VISIT CAGAGGGTTCT CTGGATGATC AAACCGGAAAC TTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE PTO AND LIVE PTO AND LIVE GIN VISIT CAGAGGGTTCT CTGGATGATC AAACCGGAAAC TTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE PTO AND LIVE PTO AND LIVE GIN VISIT CAGAGGGTTCT CTGGATGATC AAACCGGAAAC TTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE PTO AND LIVE GIN VISIT CAGAGGGTTCT CTGGATGATC AAACCGGAAAC TTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE PTO AND LIVE GIN VISIT CAGAGGGTTCT CTGGATGATC AAACCGGAAAC TTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE GIN VISIT CAGAGGAAAC TTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE GIN VISIT CAGAGGAAAC TTGTGGTTTT TAAGTTGTTT LIVE GUI PTO AND LIVE GIN VISIT CAGAGGAAAC TTGTGGTTTT LIVE GIN VISIT CAGAGGAAAC TTGTGGTTTT LIVE GIN VISIT CAGAGGAAAC T
2001 +1 2051 +1 2101 +1 2151 +1 2201 +1 2251	LIST LEU ASP PTO LIS GLU VI ASP LIS AND LIS LIS GLU SET SET ASP GLU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GLU HIS SET LEU LIS GIN PRE SET GLY PTO ASP PTO LEU SET ATTCTCATGGA GCACTCCTGAGC CTAGAGTACCT CGTGAGAGAAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PTO LEU HIE LIS LEU AIS VIS GU APP AGATCAAACTT CTAGCTTGCT TTACCCACTC ATAAAACTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AAATGGACAGA GAATGGGTGAG TATTTTGAAC GTCATCTTCG AAATGGACAGA GAATGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIE PTO ASP VIS LEU PTO TIT GN HIE TY PTO LEU PTO LIS GN GIN ASP TIT LIS AND TIT LIS AND SET TIT LIS AND TIT LIS AND SET TIT LIS AND TIT LIS AND SET TIT LIS AND SET TIT LIS AND SET TIT LIS AND SET TIT LIS GU PTO AND LEU LIS FIR GN SET LEU LIS GN VIS LIS LIS SET AND LEU LIS GN VIS LIS GN VIS LIS LIS SET AND LEU LIS GN VIS LIS GN VIS LIS LIS SET AND LEU LIS GN VIS LIS GN VIS LIS LIS LIS SET AND LEU LIS GN VIS LIS LIS LIS LIS LIS SET AND LEU LIS GN VIS LIS LIS LIS LIS LIS LIS LIS LIS LIS L
2001 +1 2051 +1 2101 +1 2151 +1 2201 +1 2251 +1 2301	LIVE LEU ASP PTO LIS GLU VII ASP LIS AND LIS LIS GLU SET SET ASP GLU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GLU HIS SET LEU LIS GIN PRE SET GLY PTO ASP PTO LEU SET ATTCTCATGGA GCACTCCTCT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PTO LEU IIIE LIS LEU AIS VIS GU APP AGTACTAGT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AAATTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIE PTO ASP VIS LEU PTO TIT GIN III NAS ASP GLY PTO LIS PTO LIS GON GIN ASP TTTCCTGATGT TCTGCCTACT CAGATCTAC CTCTCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTAGATAG GAGGGGGTT CGTCGTTTG LIS PTO LIS AG PTO TIT SET LEU PTO LEU ASP TIT LIS ASP SET TIT LIS GU PTO AG LEU LIS GIN VIS GU PTO AG LEU LIS PTO LIS ASP TIT LIS GU PTO AG LEU LIS GIN VIS GU PTO AG LEU LIS PTO GAGGGAAAC TTTGGCTTTT TAAGTTGTTT LIS GU PTO AG LEU LIS PTO GAGGGAAAC TTTGGGTTTT TAAGTTGTTT LIS GU PTO AG LEU LIS PTO GAGGAAAC TTTGGGTTTT TAAGTTGTTT LIS GU PTO AG LEU LIS PTO GAGGAAAC TTTGAAACAAC TTGAAACAAC TTGAAACTTGTTC A
2001 +1 2051 +1 2101 +1 2251 +1 2301 +1	LIVE LEU ASP PTO LIS GIU VI ASP LIS AND LIS LIS GIU SI SI ASP ASP GIU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU MI GU HIS SI LEU LIS GIN PRE SI GIV PTO ASP PTO LEU SI ATCTCATGGA GCACTCTCTT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SI TH SI SI SI SI LEU LEU TY PTO LEU IIIE LIS LEU AIS VIS GIU AIP AGTACTAGTT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AIS TH GIV GIN ASP PTE TH GIN TH AIS ASN GIV GIN AIS OS LEU LE AACTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT TIE PTO ASP VIS LEU PTO TH GIN IIE TY PTO LEU PTO LIS GIN GIN ASN TTCCTGATGT TCTGCCTACT CAGATCTATC CTCTCCCCAA GCAGCAGAAC AAAGGACTACA AGACGGATGA GTCTAGATAG GAGAGGGGTT CGTCGTTTG LEU PTO LIS ATG PTO TH SI LEU PTO LEU ASN TH LIS ASN SI TH LIS CTTCCCAAGA GACCTACTAG TTTGCCTTTG AACACCAAAA ATTCAACAAA GAAGGGTTCT CTGGATGATC AAACGGAAAC TTGTGGTTTT TAAGTTGTTT LIS GIU PTO ATG LEU LIS PTE GIV SI LIS HIS LIS SI ASN LEU LIS GIN VIS AGAGCCCCGG CTAAAATTTG GCAGCAAGCA CAAATCAAAC TTGAAACAAG TCTCGGGGCC GATTTTAAAC CGTCGTTCGT GTTTAGTTTG AACTTTGTTC VIS GIU TH GIV VIS AIS LIS ME ASN TH IIE ASN AIS AIS GIU PTO HIS
2001 +1 2051 +1 2101 +1 2151 +1 2201 +1 2251 +1 2301	LIVE LEU ASP PTO LIS GLU VII ASP LIS AND LIS LIS GLU SET SET ASP GLU ASP GCTAGACCCA AAAGAAGTTG ATAAGAACCT CAAGGAAAGC TCTGATGAGA CGATCTGGGT TTTCTTCAAC TATTCTTGGA GTTCCTTTCG AGACTACTCT ASP LEU ME GLU HIS SET LEU LIS GIN PRE SET GLY PTO ASP PTO LEU SET ATTCTCATGGA GCACTCCTCT AAACAGTTCA GTGGCCCAGA CCCACTGAGC TAGAGTACCT CGTGAGAGAA TTTGTCAAGT CACCGGGTCT GGGTGACTCG SET TIT SET SET SET LEU LEU TY PTO LEU IIIE LIS LEU AIS VIS GU APP AGTACTAGT CTAGCTTGCT TTACCCACTC ATAAAACCTTG CAGTAGAAGC TCATGATCAA GATCGAACGA AATGGGTGAG TATTTTGAAC GTCATCTTCG AAATTGGACAG CAGGACTTCA CACAGACTGC AAATGGCCAA GCATGTTTGA TTGACCTGTC GTCCTGAAGT GTGTCTGACG TTTACCCGGTT CGTACAAACT LIE PTO ASP VIS LEU PTO TIT GIN III NAS ASP GLY PTO LIS PTO LIS GON GIN ASP TTTCCTGATGT TCTGCCTACT CAGATCTAC CTCTCCCCAA GCAGCAGAAC AAGGGACTACA AGACGGATGA GTCTAGATAG GAGGGGGTT CGTCGTTTG LIS PTO LIS AG PTO TIT SET LEU PTO LEU ASP TIT LIS ASP SET TIT LIS GU PTO AG LEU LIS GIN VIS GU PTO AG LEU LIS PTO LIS ASP TIT LIS GU PTO AG LEU LIS GIN VIS GU PTO AG LEU LIS PTO GAGGGAAAC TTTGGCTTTT TAAGTTGTTT LIS GU PTO AG LEU LIS PTO GAGGGAAAC TTTGGGTTTT TAAGTTGTTT LIS GU PTO AG LEU LIS PTO GAGGAAAC TTTGGGTTTT TAAGTTGTTT LIS GU PTO AG LEU LIS PTO GAGGAAAC TTTGAAACAAC TTGAAACAAC TTGAAACTTGTTC A

+1	Val Val Thr Val Thr Mat Asn Gly Val Aka Gly Ang Asn His Ser Val Asn
2401	GTGGTGACAG TCACCATGAA TGGTGTGGCA GGTAGAAACC ACAGTGTTAA
	CACCACTGTC AGTGGTACTT ACCACACCGT CCATCTTTGG TGTCACAATT
+1	Asn Ser His Ala Ala Thr Thr Gin Tyr Ala Asn Ang Thr Val Leu Ser Gly Gin
2451	CTCCCATGCT GCCACAACCC AATATGCCAA TAGGACAGTA CTATCTGGCC
	GAGGGTACGA CGGTGTTGGG TTATACGGTT ATCCTGTCAT GATAGACCGG
+1	Gin Thr Thr Asn lile Val Thr His Arg Ala Gin Giu Mat Lau Gin Asn Gin
2501	AAACAACCAA CATAGTGACA CATAGGGCCC AAGAAATGTT GCAGAATCAG
	TTTGTTGGTT GTATCACTGT GTATCCCGGG TTCTTTACAA CGTCTTAGTC
+1	Phe lie Gly Giu Asp Thr Arg Leu Asn lie Asn Ser Ser Pro Asp Giu His
2551	TTTATTGGTG AGGACACCCG GCTGAATATT AATTCCAGTC CTGATGAGCA
	AAATAACCAC TCCTGTGGGC CGACTTATAA TTAAGGTCAG GACTACTCGT
+1	His Glu Pro Leu Leu Arg Arg Glu Gin Gin Ala Gly His Asp Glu Gly Val Leu
2601	TGAGCCTTTA CTGAGACGAG AGCAACAAGC TGGCCATGAT GAAGGTGTTC
	ACTCGGAAAT GACTCTGCTC TCGTTGTTCG ACCGGTACTA CTTCCACAAG
+1	Leu Asp Ang Leu Val Asp Ang Ang Giu Ang Pro Leu Giu Gly Gly Ang Thr
2651	TGGATCGTCT TGTGGACAGG AGGGAACGGC CACTAGAAGG TGGCCGAACT
	ACCTAGCAGA ACACCTGTCC TCCCTTGCCG GTGATCTTCC ACCGGCTTGA
+1	Asn Ser Asn Asn Asn Asn Ser Asn Pro Cys Ser Glu Gin Asp Val Leu Ala
2701	AATTCCAATA ACAACAACAG CAATCCATGT TCAGAACAAG ATGTTCTTGC
_	TTAAGGTTAT TGTTGTTGTC GTTAGGTACA AGTCTTGTTC TACAAGAACG
	Ala Gin Gly Val Pro Ser Thr Ala Ala Asp Pro Gly Pro Ser Lys Pro Arg Arg
2751	ACAGGGTGTT CCAAGCACAG CAGCAGATCC TGGGCCATCA AAGCCCAGAA
+1	TGTCCCACAA GGTTCGTGTC GTCGTCTAGG ACCCGGTAGT TTCGGGTCTT Ang Ala Gin Ang Pro Asn Ser Lau Asp Lau Ser Ala Tir Asn Vai Lau Asp
2801	GAGCACAGAG GCCTAATTCT CTGGATCTTT CAGCCACAAA TGTCCTGGAT CTCGTGTCTC CGGATTAAGA GACCTAGAAA GTCGGTGTTT ACAGGACCTA
+1	Gly Sør Sør lie Gln lie Gly Giu Sør Titr Gin Asp Gly Lys Sør Gly Sør
2851	GGCAGCAGTA TACAGATAGG TGAGTCAACA CAAGATGGCA AATCAGGATC
2031	CCGTCGTCAT ATGTCTATCC ACTCAGTTGT GTTCTACCGT TTAGTCCTAG
+1	Ser Giy Giu Lys lie Lys Lys Arg Val Lys Thr Pro Tyr Ser Leu Lys Arg Trp
2901	AGGTGAAAAG ATCAAGAAAC GTGTGAAAAC TCCCTATTCT CTTAAGCGGT
	TCCACTTTTC TAGTTCTTTG CACACTTTTG AGGGATAAGA GAATTCGCCA
+1	-Trip Arg Pho Ser Thr Trip Val lile Ser Thr Giu Ser Leu Asp Oys Giu Val
2951	GGCGCCCCTC CACCTGGGTC ATCTCCACTG AATCGCTGGA CTGTGAAGTC
	CCGCGGGGAG GTGGACCCAG TAGAGGTGAC TTAGCGACCT GACACTTCAG
+1	Asn Asn Asn Gily Ser Asn Arg Ala Val His Ser Lys Ser Ser Trr Ala Val-
3001	AACAATAATG GCAGTAACAG GGCAGTTCAT TCCAAATCCA GCACTGCTGT
	TTGTTATTAC CGTCATTGTC CCGTCAAGTA AGGTTTAGGT CGTGACGACA
+1	-Val Tyr Leu Ala Giu Gly Gly Thr Ala Thr Thr Met Val Ser Lys Asp lie Gly
3051	TTACCTTGCA GAAGGAGGCA CTGCTACAAC CATGGTGTCT AAAGATATAG
	AATGGAACGT CTTCCTCCGT GACGATGTTG GTACCACAGA TTTCTATATC
+1	Gly Mat Asn Cys Leu ***
3101	GAATGAACTG TCTGTGA
	CTTACTTGAC AGACACT